



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/032,201A
Source: OIP
Date Processed by STIC: 4/24/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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OIPE

Does Not Comply
Corrected Diskette Needed
See p. 6

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/032,201A

DATE: 04/24/2002
TIME: 10:57:50

Input Set : A:\351bseq.002
Output Set: N:\CRF3\04242002\J032201A.raw

3 <110> APPLICANT: Van Rooijen, Gijs
4 Deckers, Harm
5 Heifetz, Peter Bernard
6 Briggs, Steven
7 Dalmia, Bipin Kumar
8 Del Val, Greg
9 Zaplachinski, Steve
10 Moloney, Maurice
12 <120> TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND
RELATED
13 COMPOSITIONS
15 <130> FILE REFERENCE: 38814-351B
17 <140> CURRENT APPLICATION NUMBER: 10/032,201A
C--> 18 <141> CURRENT FILING DATE: 2002-04-09
20 <160> NUMBER OF SEQ ID NOS: 313
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 22
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Primer
32 <400> SEQUENCE: 1
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35 <210> SEQ ID NO: 2
36 <211> LENGTH: 22
37 <212> TYPE: DNA
38 <213> ORGANISM: Artificial Sequence
40 <220> FEATURE:
41 <223> OTHER INFORMATION: Primer
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46 <210> SEQ ID NO: 3
47 <211> LENGTH: 36
48 <212> TYPE: DNA
49 <213> ORGANISM: Artificial Sequence
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52 <223> OTHER INFORMATION: Primer
54 <400> SEQUENCE: 3
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57 <210> SEQ ID NO: 4
58 <211> LENGTH: 28
59 <212> TYPE: DNA
60 <213> ORGANISM: Artificial Sequence

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Input Set : A:\351bseq.002

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63 <223> OTHER INFORMATION: Primer
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69 <211> LENGTH: 72
70 <212> TYPE: DNA
71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: Primer
76 <400> SEQUENCE: 5
77 actggagatg ttgactcgac ggatactacg gattggctga cggctatgga agaaggacaa 60
78 gtgacgcct gc 72
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81 <211> LENGTH: 80
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: Primer
88 <400> SEQUENCE: 6
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90 ctcttgtaag aatgctctgc 80
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93 <211> LENGTH: 22
94 <212> TYPE: DNA
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <223> OTHER INFORMATION: Primer
100 <400> SEQUENCE: 7
101 gtggaagctt atggagatgg ag 22
103 <210> SEQ ID NO: 8
104 <211> LENGTH: 1002
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Chimeric
111 <400> SEQUENCE: 8
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113 cacacggcgg cgatttacgc agctagggtc gaacttaaac ctcttctctt cgaaggatgg 120
114 atggctaacg acatcgctcc cgggtggtcaa ctaacaacca ccaccgacgt cgagaatttc 180
115 cccggatttc cagaaggtat tctcggagta gagctcactg acaaattccg taaacaatcg 240
116 gagcgattcg gtactacgat atttacagag acggtgacga aagtcgattt ctcttcgaaa 300
117 ccgtttaagc tattcacaga ttcaaaagcc attctcgtcg acgctgtgat tctcgtact 360
118 ggagctgtgg ctaagcggct tagcttcggt ggatctggtg aaggttctgg aggttctg 420
119 aaccgtggaa tctccgcttg tgctgtttgc gacggagctg ctccgatatt ccgtaacaaa 480
120 cctcttgccg tgatcgggtg aggcgattca gcaatggaag aagcaaactt tcttacaaaa 540
121 tatggatcta aagtgtatat aatccatagg agagatgctt ttagagcgtc taagattatg 600
122 cagcagcgag ctttgtctaa tctaagatt gatgtgattt ggaactcgtc tgttggtgaa 660
123 gcttatggag atggagaaa agatgtgctt ggaggattga aagtgaagaa tgtggttacc 720

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Input Set : A:\351bseq.002

Output Set: N:\CRF3\04242002\J032201A.raw

124 ggagatgttt ctgatttaaa agtttctgga ttgttctttg ctattggtca tgagccagct 780
125 accaagtttt tggatggtgg tggttgagttta gattcggatg gttatgttgt cacgaagcct 840
126 ggtactacac agactagcgt tcccggagtt ttcgctgcgg gtgatgttca ggataagaag 900
127 tataggcaag ccatcactgc tgcaggaact ggggtgcatgg cagctttgga tgcagagcat 960
128 tactttacaag agattggatc tcagcaaggt aagagtgatt ga 1002

130 <210> SEQ ID NO: 9

131 <211> LENGTH: 999

132 <212> TYPE: DNA

133 <213> ORGANISM: Arabidopsis thaliana

135 <400> SEQUENCE: 9

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137 cacacggcgg cgatttacgc agctagggct gaacttaaac ctcttctctt cgaaggatgg 120
138 atggctaacg acatcgctcc cgggtggtcaa ctcaaccaac caccgcgtga gaatttccc 180
139 ggatttccag aaggtattct cggagtagag ctcaactgaca aattccgtaa acaatcggag 240
140 cgattcggta ctacgatatt tacagagacg gtgacgaaag tcgatttctc ttcgaaaccg 300
141 ttttaagctat tcacagattc aaaagccatt ctgctgacg ctgtgattct cgctatcgga 360
142 gctgtggcta agtggcttag ctctgttggg tctgtggaag ttctcggagg tttgtggaac 420
143 cgtggaatct ccgcttgcgc tggttgccgc ggagctgctc cgatattccg caacaaacct 480
144 cttgcgggtga tcggtggagg cgattctgca atggaagaag caaactttct taaaaatat 540
145 ggatctaaag tgtatataat cgataggaga gatgcttcta gagcgtctaa gattatgcag 600
146 cagcgaagctt tgtctaattc taagattgat gtgatttggg actcgtctgt tgtggaagct 660
147 tatggagatg gagaaagaga tgtgcttggg ggattgaaag tgaagaatgt ggttaccgga 720
148 gatgtttctg atttaaaagt ttctggattg ttctttgcta ttggtcatga gccagctacc 780
149 aagtttttgg atggtggtgt tgagttagat tcggatggtt atgttgctac gaagcctggt 840
150 actacacaga ctagegttcc cggagttttc gctgcgggtg atgttcagga taagaagtat 900
151 aggaagcca tcaactgctc aggaactggg tgcattggcag ctttggatgc agagcattac 960
152 ttacaagaga ttggatctca gcaaggttaag agtgattga 999

154 <210> SEQ ID NO: 10

155 <211> LENGTH: 1002

156 <212> TYPE: DNA

157 <213> ORGANISM: Artificial Sequence

159 <220> FEATURE:

160 <223> OTHER INFORMATION: Chimeric

W--> 162 <221> NAME/KEY: CDS

163 <222> LOCATION: (1)...(1002)

164 <223> OTHER INFORMATION: cDNA encoding NADPH thioredoxin reductase

W--> 166 <400> 10

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168 Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
169 1 5 10 15
171 ggc cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt 96
172 Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
173 20 25 30
175 aaa cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt 144
176 Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
177 35 40 45
179 ggt caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca 192
180 Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
181 50 55 60

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Input Set : A:\351bseq.002

Output Set: N:\CRF3\04242002\J032201A.raw

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183 gaa ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg      240
184 Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
185 65                               70                               75                               80
187 gag cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat      288
188 Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
189                               85                               90                               95
191 ttc tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc      336
192 Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
193                               100                              105                              110
195 gct gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc      384
196 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
197                               115                              120                              125
199 ttc gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc      432
200 Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
201                               130                              135                              140
203 tcc gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa      480
204 Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
205 145                               150                               155                               160
207 cct ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac      528
208 Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
209                               165                              170                              175
211 ttt ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat      576
212 Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
213                               180                              185                              190
215 gct ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct      624
216 Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
217                               195                              200                              205
219 aag att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat      672
220 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
221                               210                              215                              220
223 gga gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc      720
224 Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
225 225                               230                              235                              240
227 gga gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt      768
228 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
229                               245                              250                              255
231 cat gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg      816
232 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
233                               260                              265                              270
235 gat ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc      864
236 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
237                               275                              280                              285
239 gga gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc      912
240 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
241                               290                              295                              300
243 atc act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat      960
244 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
245 305                               310                              315                              320
247 tac tta caa gag att gga tct cag caa ggt aag agt gat tga      1002

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248 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp *
249 325 330
253 <210> SEQ ID NO: 11
254 <211> LENGTH: 333
255 <212> TYPE: PRT
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Chimeric
261 <400> SEQUENCE: 11
262 Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
263 1 5 10 15
264 Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
265 20 25 30
266 Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
267 35 40 45
268 Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
269 50 55 60
270 Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
271 65 70 75 80
272 Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
273 85 90 95
274 Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
275 100 105 110
276 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
277 115 120 125
278 Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
279 130 135 140
280 Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
281 145 150 155 160
282 Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
283 165 170 175
284 Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
285 180 185 190
286 Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
287 195 200 205
288 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
289 210 215 220
290 Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
291 225 230 235 240
292 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
293 245 250 255
294 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
295 260 265 270
296 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
297 275 280 285
298 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
299 290 295 300
300 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
301 305 310 315 320

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/032,201A

DATE: 04/24/2002
TIME: 10:57:51

Input Set : A:\351bseq.002
Output Set: N:\CRF3\04242002\J032201A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:101; Xaa Pos. 16,17,38,42,45,54,55,58,66,72,75,79,80,81,94,99,103
Seq#:109; Xaa Pos. 17,38,42,55,58,60,72,107
Seq#:134; Xaa Pos. 21,35
Seq#:245; Xaa Pos. 33,45,46
Seq#:275; Xaa Pos. 9,11
Seq#:287; Xaa Pos. 524
Seq#:288; Xaa Pos. 666
Seq#:290; Xaa Pos. 523
Seq#:293; Xaa Pos. 520
Seq#:294; Xaa Pos. 578
Seq#:295; Xaa Pos. 523
Seq#:296; Xaa Pos. 576
Seq#:300; Xaa Pos. 612
Seq#:303; Xaa Pos. 523
Seq#:304; Xaa Pos. 527
Seq#:307; Xaa Pos. 497
Seq#:309; Xaa Pos. 497
Seq#:312; Xaa Pos. 525
Seq#:313; Xaa Pos. 498

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:10,16,17,18,19,22,24,27,30,33,34,35

VERIFICATION SUMMARY

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Input Set : A:\351bseq.002

Output Set: N:\CRF3\04242002\J032201A.raw

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:162 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:166 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:538 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:541 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:544 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:680 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:680 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:704 M:258 W: Mandatory Feature missing, <220> FEATURE:
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L:737 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:740 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:743 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:856 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:945 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:948 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:22
L:1151 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:24
L:1434 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1437 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:27
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L:2066 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:2297 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:34
L:2330 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:35
L:2334 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:35
L:2340 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:35
L:4706 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:0
L:4708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:16
L:4710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:32
L:4712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:48
L:4714 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:64
L:4716 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:80
L:4718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:101 after pos.:96
L:4895 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109 after pos.:16
L:4897 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109 after pos.:32
L:4899 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109 after pos.:48
L:4901 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109 after pos.:64
L:4905 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109 after pos.:96
L:5488 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:134 after pos.:16
L:5490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:134 after pos.:32
L:9690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:245 after pos.:32
L:11041 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:275 after pos.:0
L:11598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:287 after pos.:512
L:11695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:288 after pos.:656
L:11848 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:290 after pos.:512
L:12071 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:293 after pos.:512
L:12158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:294 after pos.:576
L:12237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:295 after pos.:512

VERIFICATION SUMMARY

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Input Set : A:\351bseq.002

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L:12322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:296 after pos.:560
L:12637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:300 after pos.:608
L:12850 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:303 after pos.:512
L:12929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:304 after pos.:512
L:13152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:307 after pos.:496
L:13259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:309 after pos.:496
L:13418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:312 after pos.:512
L:13495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:313 after pos.:496